#9

SEQUENCE LISTING

<110> Droux, Michel
       DeRose, Richard
       Job, Dominque

<120> Method for Increasing the Content of Sulphur Compounds
       and In Particular of Cysteine, Methionine and
       Glutathione in Plants and Plants Obtained

<130> 5500*42

<140> 09/486,334
<141> 2001-07-11

<160> 23

<170> PatentIn Ver. 2.0

<210> 1
<211> 984
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (31)..(972)

<400> 1
gagagaggat cctctttcca atcataaacc atg gca aca tgc ata gac aca tgc   54
                                  Met Ala Thr Cys Ile Asp Thr Cys
                                   1   5

cga acc ggt aat acc caa gac gat gat tcc cgg ttc tgt tgc atc aag 102
Arg Thr Gly Asn Thr Gln Asp Asp Asp Ser Arg Phe Cys Cys Ile Lys
    10   15   20

aat ttc ttt cga ccc ggt ttc tct gta aac cgg aag att cac cac acc 150
Asn Phe Phe Arg Pro Gly Phe Ser Val Asn Arg Lys Ile His His Thr
25   30   35   40

caa atc gaa gat gac gat gat gtc tgg atc aag atg ctt gaa gaa gcc 198
Gln Ile Glu Asp Asp Asp Asp Val Trp Ile Lys Met Leu Glu Glu Ala
                45   50   55

aaa tcc gat gtt aaa caa gaa ccc att tta tca aac tac tac tac gct 246
Lys Ser Asp Val Lys Gln Glu Pro Ile Leu Ser Asn Tyr Tyr Tyr Ala
                60   65   70

tcg atc aca tct cat cga tct tta gag tct gct tta gct cac atc ctc   294
Ser Ile Thr Ser His Arg Ser Leu Glu Ser Ala Leu Ala His Ile Leu
        75   80   85

tcc gta aag ctc agc aat tta aac cta cca agc aac aca ctc ttc gaa   342
Ser Val Lys Leu Ser Asn Leu Asn Leu Pro Ser Asn Thr Leu Phe Glu
        90   95   100

ctg ttc ata agc gtt tta gaa gaa agc cct gag atc atc gaa tcc acg   390
Leu Phe Ile Ser Val Leu Glu Glu Ser Pro Glu Ile Ile Glu Ser Thr
105   110   115   120

aag caa gat ctt ata gca gtc aaa gaa aga gac cca gct tgt ata agc   438
Lys Gln Asp Leu Ile Ala Val Lys Glu Arg Asp Pro Ala Cys Ile Ser
                125   130   135

tac gtt cat tgc ttc ttg ggc ttc aaa ggc ttc ctc gct tgt caa gct   486
Tyr Val His Cys Phe Leu Gly Phe Lys Gly Phe Leu Ala Cys Gln Ala
                140   145   150

cat cga ata gct cat acc ctc tgg aaa cag aac aga aaa atc gta gct   534
His Arg Ile Ala His Thr Leu Trp Lys Gln Asn Arg Lys Ile Val Ala
                155   160   165

tta ttg atc caa aac aga gta tca gaa tct ttc gcc gtc gat att cat   582
Leu Leu Ile Gln Asn Arg Val Ser Glu Ser Phe Ala Val Asp Ile His
        170   175   180

ccc gga gcg aag atc gga aaa ggg att ctt tta gac cat gcg acg ggc   630
Pro Gly Ala Lys Ile Gly Lys Gly Ile Leu Leu Asp His Ala Thr Gly
185   190   195   200

gtg gtg atc gga gag acg gcg gtg gtt gga gac aat gtt tcg att cta   678
Val Val Ile Gly Glu Thr Ala Val Val Gly Asp Asn Val Ser Ile Leu
                205   210   215

cac gga gtg acc ttg gga gga aca ggg aaa cag agt ggt gat cgg cat   726
His Gly Val Thr Leu Gly Gly Thr Gly Lys Gln Ser Gly Asp Arg His
                220   225   230

ccg aag att ggt gat ggt gtg ttg att gga gct ggg agt tgt ata ttg   774
Pro Lys Ile Gly Asp Gly Val Leu Ile Gly Ala Gly Ser Cys Ile Leu
                235   240   245

ggg aat ata aca atc ggt gag gga gct aag att gga tca ggg tcg gtg   822
Gly Asn Ile Thr Ile Gly Glu Gly Ala Lys Ile Gly Ser Gly Ser Val
        250   255   260

2

```
gtg gtt aag gat gtg ccg gcg cgt acg acg gcg gtt gga aat ccg gcg   870
Val Val Lys Asp Val Pro Ala Arg Thr Thr Ala Val Gly Asn Pro Ala
265             270             275             280

agg ttg att ggt ggg aaa gag aat ccg aga aaa cat gat aag att cct   918
Arg Leu Ile Gly Gly Lys Glu Asn Pro Arg Lys His Asp Lys Ile Pro
                285             290             295

tgt ctg act atg gac cag aca tcg tat tta acc gag tgg tct gat tat   966
Cys Leu Thr Met Asp Gln Thr Ser Tyr Leu Thr Glu Trp Ser Asp Tyr
                300             305             310

gtg att taacacaaat gt                                              984
Val Ile
```

<210> 2
<211> 314
<212> PRT
<213> Arabidopsis thaliana

```
<400> 2
Met Ala Thr Cys Ile Asp Thr Cys Arg Thr Gly Asn Thr Gln Asp Asp
 1               5              10              15

Asp Ser Arg Phe Cys Cys Ile Lys Asn Phe Phe Arg Pro Gly Phe Ser
            20              25              30

Val Asn Arg Lys Ile His His Thr Gln Ile Glu Asp Asp Asp Asp Val
            35              40              45

Trp Ile Lys Met Leu Glu Glu Ala Lys Ser Asp Val Lys Gln Glu Pro
        50              55              60

Ile Leu Ser Asn Tyr Tyr Tyr Ala Ser Ile Thr Ser His Arg Ser Leu
 65              70              75              80

Glu Ser Ala Leu Ala His Ile Leu Ser Val Lys Leu Ser Asn Leu Asn
                85              90              95

Leu Pro Ser Asn Thr Leu Phe Glu Leu Phe Ile Ser Val Leu Glu Glu
            100             105             110

Ser Pro Glu Ile Ile Glu Ser Thr Lys Gln Asp Leu Ile Ala Val Lys
        115             120             125

Glu Arg Asp Pro Ala Cys Ile Ser Tyr Val His Cys Phe Leu Gly Phe
```

```
                    130              135              140

Lys Gly Phe Leu Ala Cys Gln Ala His Arg Ile Ala His Thr Leu Trp
145              150              155              160

Lys Gln Asn Arg Lys Ile Val Ala Leu Leu Ile Gln Asn Arg Val Ser
                 165              170              175

Glu Ser Phe Ala Val Asp Ile His Pro Gly Ala Lys Ile Gly Lys Gly
                 180              185              190

Ile Leu Leu Asp His Ala Thr Gly Val Val Ile Gly Glu Thr Ala Val
                 195              200              205

Val Gly Asp Asn Val Ser Ile Leu His Gly Val Thr Leu Gly Gly Thr
                 210              215              220

Gly Lys Gln Ser Gly Asp Arg His Pro Lys Ile Gly Asp Gly Val Leu
225              230              235              240

Ile Gly Ala Gly Ser Cys Ile Leu Gly Asn Ile Thr Ile Gly Glu Gly
                 245              250              255

Ala Lys Ile Gly Ser Gly Ser Val Val Val Lys Asp Val Pro Ala Arg
                 260              265              270

Thr Thr Ala Val Gly Asn Pro Ala Arg Leu Ile Gly Gly Lys Glu Asn
                 275              280              285

Pro Arg Lys His Asp Lys Ile Pro Cys Leu Thr Met Asp Gln Thr Ser
    290              295              300

Tyr Leu Thr Glu Trp Ser Asp Tyr Val Ile
305              310
```

```
<210> 3
<211> 974
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (31)..(966)

<400> 3
gagagaggat cctcttatcg ccgcgttaat atg cca ccg gcc gga gaa ctc cga    54
                                    Met Pro Pro Ala Gly Glu Leu Arg
```

```
cat caa tct cca tca aag gag aaa cta tct tcc gtt acc caa tcc gat   102
His Gln Ser Pro Ser Lys Glu Lys Leu Ser Ser Val Thr Gln Ser Asp
     10          15              20

gaa gca gaa gca gcg tca gca gcg ata tct gcg gca gct gca gat gcg   150
Glu Ala Glu Ala Ala Ser Ala Ala Ile Ser Ala Ala Ala Ala Asp Ala
 25              30              35              40

gaa gct gcc gga tta tgg aca cag atc aag gcg gaa gct cgc cgt gat   198
Glu Ala Ala Gly Leu Trp Thr Gln Ile Lys Ala Glu Ala Arg Arg Asp
             45              50              55

gct gag gcg gag cca gct tta gct agc tat cta tat tcg acg att ctt   246
Ala Glu Ala Glu Pro Ala Leu Ala Ser Tyr Leu Tyr Ser Thr Ile Leu
             60              65              70

tct cat tcg tct ctt gaa cga tct atc tcg ttt cat cta gga aac aag   294
Ser His Ser Ser Leu Glu Arg Ser Ile Ser Phe His Leu Gly Asn Lys
             75              80              85

ctt tgt tcc tca acg ctt tta tcc aca ctt tta tac gat ctg ttc tta   342
Leu Cys Ser Ser Thr Leu Leu Ser Thr Leu Leu Tyr Asp Leu Phe Leu
     90              95              100

aac act ttt tcc tcc gat cct tct ctt cgt aac gcc acc gtc gca gat   390
Asn Thr Phe Ser Ser Asp Pro Ser Leu Arg Asn Ala Thr Val Ala Asp
105             110             115             120

cta cgc gct gct cgt gtt cgt gat cct gct tgt atc tcg ttc tct cat   438
Leu Arg Ala Ala Arg Val Arg Asp Pro Ala Cys Ile Ser Phe Ser His
             125             130             135

tgt ctc ctc aat tac aaa ggc ttc tta gct att cag gcg cat cgt gta   486
Cys Leu Leu Asn Tyr Lys Gly Phe Leu Ala Ile Gln Ala His Arg Val
             140             145             150

tca cac aag cta tgg aca caa tca cgg aag cca tta gca tta gct cta   534
Ser His Lys Leu Trp Thr Gln Ser Arg Lys Pro Leu Ala Leu Ala Leu
             155             160             165

cac tca aga atc tcc gat gta ttc gct gtt gat atc cat cca gca gcg   582
His Ser Arg Ile Ser Asp Val Phe Ala Val Asp Ile His Pro Ala Ala
     170             175             180

aag atc gga aaa ggg ata ctt cta gac cac gca acc gga gtt gta gtc   630
Lys Ile Gly Lys Gly Ile Leu Leu Asp His Ala Thr Gly Val Val Val
```

```
gga gaa aca gcg gtg att ggg aac aat gtt tca atc ctt cac cat gtg    678
Gly Glu Thr Ala Val Ile Gly Asn Asn Val Ser Ile Leu His His Val
            205                    210                    215

aca cta ggt gga aca ggt aaa gct tgt gga gat aga cat ccg aag atc    726
Thr Leu Gly Gly Thr Gly Lys Ala Cys Gly Asp Arg His Pro Lys Ile
            220                    225                    230

ggt gac ggt tgt ttg att gga gct gga gcg act att ctt gga aat gtg    774
Gly Asp Gly Cys Leu Ile Gly Ala Gly Ala Thr Ile Leu Gly Asn Val
            235                    240                    245

aag att ggt gca ggt gct aaa gta gga gct ggt tct gtt gtg ctg att    822
Lys Ile Gly Ala Gly Ala Lys Val Gly Ala Gly Ser Val Val Leu Ile
            250                    255                    260

gac gtg cct tgt cga ggt act gcg gtt ggg aat ccg gcg aga ctt gtc    870
Asp Val Pro Cys Arg Gly Thr Ala Val Gly Asn Pro Ala Arg Leu Val
265                    270                    275                    280

gga ggg aaa gag aag cca acg att cat gat gag gaa tgt cct gga gaa    918
Gly Gly Lys Glu Lys Pro Thr Ile His Asp Glu Glu Cys Pro Gly Glu
            285                    290                    295

tcg atg gat cat act tca ttc atc tcg gaa tgg tca gat tac atc ata    966
Ser Met Asp His Thr Ser Phe Ile Ser Glu Trp Ser Asp Tyr Ile Ile
            300                    305                    310

taaagttg
                                                                   974
```

<210> 4
<211> 312
<212> PRT
<213> Arabidopsis thaliana

<400> 4

```
Met Pro Pro Ala Gly Glu Leu Arg His Gln Ser Pro Ser Lys Glu Lys
1               5                   10                  15

Leu Ser Ser Val Thr Gln Ser Asp Glu Ala Glu Ala Ala Ser Ala Ala
            20                  25                  30

Ile Ser Ala Ala Ala Ala Asp Ala Glu Ala Ala Gly Leu Trp Thr Gln
        35                  40                  45
```

```
Ile Lys Ala Glu Ala Arg Arg Asp Ala Glu Ala Glu Pro Ala Leu Ala
    50                  55                  60

Ser Tyr Leu Tyr Ser Thr Ile Leu Ser His Ser Ser Leu Glu Arg Ser
    65                  70                  75                  80

Ile Ser Phe His Leu Gly Asn Lys Leu Cys Ser Ser Thr Leu Leu Ser
                85                  90                  95

Thr Leu Leu Tyr Asp Leu Phe Leu Asn Thr Phe Ser Ser Asp Pro Ser
                100                 105                 110

Leu Arg Asn Ala Thr Val Ala Asp Leu Arg Ala Ala Arg Val Arg Asp
                115                 120                 125

Pro Ala Cys Ile Ser Phe Ser His Cys Leu Leu Asn Tyr Lys Gly Phe
    130                 135                 140

Leu Ala Ile Gln Ala His Arg Val Ser His Lys Leu Trp Thr Gln Ser
    145                 150                 155                 160

Arg Lys Pro Leu Ala Leu Ala Leu His Ser Arg Ile Ser Asp Val Phe
                165                 170                 175

Ala Val Asp Ile His Pro Ala Ala Lys Ile Gly Lys Gly Ile Leu Leu
                180                 185                 190

Asp His Ala Thr Gly Val Val Val Gly Glu Thr Ala Val Ile Gly Asn
                195                 200                 205

Asn Val Ser Ile Leu His His Val Thr Leu Gly Gly Thr Gly Lys Ala
    210                 215                 220

Cys Gly Asp Arg His Pro Lys Ile Gly Asp Gly Cys Leu Ile Gly Ala
225                 230                 235                 240

Gly Ala Thr Ile Leu Gly Asn Val Lys Ile Gly Ala Gly Ala Lys Val
                245                 250                 255

Gly Ala Gly Ser Val Val Leu Ile Asp Val Pro Cys Arg Gly Thr Ala
                260                 265                 270

Val Gly Asn Pro Ala Arg Leu Val Gly Gly Lys Glu Lys Pro Thr Ile
    275                 280                 285

His Asp Glu Glu Cys Pro Gly Glu Ser Met Asp His Thr Ser Phe Ile
    290                 295                 300
```

7

Ser Glu Trp Ser Asp Tyr Ile Ile
305   310

<210> 5
<211> 1048
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (31)..(1038)

<400> 5
gagagaggat cccctcctcc tcctcctcct atg gct gcg tgc atc gac acc tgc   54
                                  Met Ala Ala Cys Ile Asp Thr Cys
                                   1   5

cgc act ggt aaa ccc cag att tct cct cgc gat tct tct aaa cac cac   102
Arg Thr Gly Lys Pro Gln Ile Ser Pro Arg Asp Ser Ser Lys His His
     10   15   20

gac gat gaa tct ggc ttt cgt tac atg aac tac ttc cgt tat cct gat   150
Asp Asp Glu Ser Gly Phe Arg Tyr Met Asn Tyr Phe Arg Tyr Pro Asp
 25   30   35   40

cga tct tcc ttc aat gga acc cag acc aaa acc ctc cat act cgt cct   198
Arg Ser Ser Phe Asn Gly Thr Gln Thr Lys Thr Leu His Thr Arg Pro
                 45   50   55

ttg ctt gaa gat ctc gat cgc gac gct gaa gtc gat gat gtt tgg gcc   246
Leu Leu Glu Asp Leu Asp Arg Asp Ala Glu Val Asp Asp Val Trp Ala
             60   65   70

aaa atc cga gaa gag gct aaa tct gat atc gcc aaa gaa cct att gtt   294
Lys Ile Arg Glu Glu Ala Lys Ser Asp Ile Ala Lys Glu Pro Ile Val
         75   80   85

tcc gct tat tat cac gct tcg att gtt tct cag cgt tcg ttg gaa gct   342
Ser Ala Tyr Tyr His Ala Ser Ile Val Ser Gln Arg Ser Leu Glu Ala
     90   95   100

gcg ttg gcg aat act tta tct gtt aaa ctc agc aat ttg aat ctt cca   390
Ala Leu Ala Asn Thr Leu Ser Val Lys Leu Ser Asn Leu Asn Leu Pro
105   110   115   120

agc aac acg ctt ttc gat ttg ttc tct ggt gtt ctt caa gga aac cca   438
Ser Asn Thr Leu Phe Asp Leu Phe Ser Gly Val Leu Gln Gly Asn Pro

8

```
gat att gtt gaa tct gtc aag cta gat ctt tta gct gtt aag gag aga   486
Asp Ile Val Glu Ser Val Lys Leu Asp Leu Leu Ala Val Lys Glu Arg
                140             145             150
```

```
gat cct gct tgt ata agc tac gtt cat tgt ttc ctt cac ttt aaa ggc   534
Asp Pro Ala Cys Ile Ser Tyr Val His Cys Phe Leu His Phe Lys Gly
            155             160             165
```

```
ttc ctc gct tgt caa gcg cat cgt att gct cat gag ctt tgg act cag   582
Phe Leu Ala Cys Gln Ala His Arg Ile Ala His Glu Leu Trp Thr Gln
        170             175             180
```

```
gac aga aaa atc cta gct ttg ttg atc cag aac aga gtc tct gaa gcc   630
Asp Arg Lys Ile Leu Ala Leu Leu Ile Gln Asn Arg Val Ser Glu Ala
185             190             195             200
```

```
ttc gct gtt gat ttc cac cct gga gct aaa atc ggt acc ggg att ttg   678
Phe Ala Val Asp Phe His Pro Gly Ala Lys Ile Gly Thr Gly Ile Leu
                205             210             215
```

```
cta gac cat gct acg gct att gtg atc ggt gag acg gcg gtt gtg ggg   726
Leu Asp His Ala Thr Ala Ile Val Ile Gly Glu Thr Ala Val Val Gly
            220             225             230
```

```
aac aat gtt tcg att ctc cat aac gtt acg ctt gga gga acg ggg aaa   774
Asn Asn Val Ser Ile Leu His Asn Val Thr Leu Gly Gly Thr Gly Lys
            235             240             245
```

```
cag tgt gga gat agg cac ccg aag att ggc gat ggg gtt ttg att gga   822
Gln Cys Gly Asp Arg His Pro Lys Ile Gly Asp Gly Val Leu Ile Gly
        250             255             260
```

```
gct ggg act tgt att ttg ggg aat atc acg att ggt gaa gga gct aag   870
Ala Gly Thr Cys Ile Leu Gly Asn Ile Thr Ile Gly Glu Gly Ala Lys
265             270             275             280
```

```
att ggt gcg ggg tcg gtg gtg ttg aaa gac gtg ccg ccg cgt acg acg   918
Ile Gly Ala Gly Ser Val Val Leu Lys Asp Val Pro Pro Arg Thr Thr
            285             290             295
```

```
gct gtt gga aat ccg gcg agg ttg ctt ggt ggt aaa gat aat ccg aaa   966
Ala Val Gly Asn Pro Ala Arg Leu Leu Gly Gly Lys Asp Asn Pro Lys
            300             305             310
```

```
acg cat gac aag att cct ggt ttg act atg gac cag acg tcg cat ata   1014
Thr His Asp Lys Ile Pro Gly Leu Thr Met Asp Gln Thr Ser His Ile
```

```
tcc gag tgg tcg gat tat gta att tgaaaaagtc                    1048
Ser Glu Trp Ser Asp Tyr Val Ile
    330                 335
```

<210> 6
<211> 336
<212> PRT
<213> Arabidopsis thaliana

<400> 6

```
Met Ala Ala Cys Ile Asp Thr Cys Arg Thr Gly Lys Pro Gln Ile Ser
 1               5                   10                  15

Pro Arg Asp Ser Ser Lys His His Asp Asp Glu Ser Gly Phe Arg Tyr
            20                  25                  30

Met Asn Tyr Phe Arg Tyr Pro Asp Arg Ser Ser Phe Asn Gly Thr Gln
        35                  40                  45

Thr Lys Thr Leu His Thr Arg Pro Leu Leu Glu Asp Leu Asp Arg Asp
    50                  55                  60

Ala Glu Val Asp Asp Val Trp Ala Lys Ile Arg Glu Glu Ala Lys Ser
65                  70                  75                  80

Asp Ile Ala Lys Glu Pro Ile Val Ser Ala Tyr Tyr His Ala Ser Ile
                85                  90                  95

Val Ser Gln Arg Ser Leu Glu Ala Ala Leu Ala Asn Thr Leu Ser Val
            100                 105                 110

Lys Leu Ser Asn Leu Asn Leu Pro Ser Asn Thr Leu Phe Asp Leu Phe
        115                 120                 125

Ser Gly Val Leu Gln Gly Asn Pro Asp Ile Val Glu Ser Val Lys Leu
    130                 135                 140

Asp Leu Leu Ala Val Lys Glu Arg Asp Pro Ala Cys Ile Ser Tyr Val
145                 150                 155                 160

His Cys Phe Leu His Phe Lys Gly Phe Leu Ala Cys Gln Ala His Arg
                165                 170                 175

Ile Ala His Glu Leu Trp Thr Gln Asp Arg Lys Ile Leu Ala Leu Leu
            180                 185                 190
```

```
Ile Gln Asn Arg Val Ser Glu Ala Phe Ala Val Asp Phe His Pro Gly
        195                 200                 205

Ala Lys Ile Gly Thr Gly Ile Leu Leu Asp His Ala Thr Ala Ile Val
        210                 215                 220

Ile Gly Glu Thr Ala Val Val Gly Asn Asn Val Ser Ile Leu His Asn
225                 230                 235                 240

Val Thr Leu Gly Gly Thr Gly Lys Gln Cys Gly Asp Arg His Pro Lys
                245                 250                 255

Ile Gly Asp Gly Val Leu Ile Gly Ala Gly Thr Cys Ile Leu Gly Asn
                260                 265                 270

Ile Thr Ile Gly Glu Gly Ala Lys Ile Gly Ala Gly Ser Val Val Leu
        275                 280                 285

Lys Asp Val Pro Pro Arg Thr Thr Ala Val Gly Asn Pro Ala Arg Leu
        290                 295                 300

Leu Gly Gly Lys Asp Asn Pro Lys Thr His Asp Lys Ile Pro Gly Leu
305                 310                 315                 320

Thr Met Asp Gln Thr Ser His Ile Ser Glu Trp Ser Asp Tyr Val Ile
                325                 330                 335
```

```
<210> 7
<211> 1213
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (31)..(1203)

<220>
<221> sig_peptide
<222> (31)..(219)

<400> 7
gagagaggat ccggccgaga aaaaaaaaaa atg ttg ccg gtc aca agt cgc cgc   54
                                  Met Leu Pro Val Thr Ser Arg Arg
                                  1               5

cac ttc aca atg tcc cta tat atg ctc cgt tca tct tct cca cac atc  102
```

```
        His Phe Thr Met Ser Leu Tyr Met Leu Arg Ser Ser Ser Pro His Ile
             10                  15                  20

aat cat cac tct ttc ctt ctt cct tct ttt gtt tcc tcc aaa ttc aaa   150
Asn His His Ser Phe Leu Leu Pro Ser Phe Val Ser Ser Lys Phe Lys
 25              30                  35                  40

cac cat act tta tct cct cct cct tct cct cct cct cct cct cct atg   198
His His Thr Leu Ser Pro Pro Pro Ser Pro Pro Pro Pro Pro Pro Met
                 45                  50                  55

gct gcg tgc atc gac acc tgc cgc act ggt aaa ccc cag att tct cct   246
Ala Ala Cys Ile Asp Thr Cys Arg Thr Gly Lys Pro Gln Ile Ser Pro
                     60                  65                  70

cgc gat tct tct aaa cac cac gac gat gaa tct ggc ttt cgt tac atg   294
Arg Asp Ser Ser Lys His His Asp Asp Glu Ser Gly Phe Arg Tyr Met
                 75                  80                  85

aac tac ttc cgt tat cct gat cga tct tcc ttc aat gga acc cag acc   342
Asn Tyr Phe Arg Tyr Pro Asp Arg Ser Ser Phe Asn Gly Thr Gln Thr
         90                  95                 100

aaa acc ctc cat act cgt cct ttg ctt gaa gat ctc gat cgc gac gct   390
Lys Thr Leu His Thr Arg Pro Leu Leu Glu Asp Leu Asp Arg Asp Ala
105                 110                 115                 120

gaa gtc gat gat gtt tgg gcc aaa atc cga gaa gag gct aaa tct gat   438
Glu Val Asp Asp Val Trp Ala Lys Ile Arg Glu Glu Ala Lys Ser Asp
                     125                 130                 135

atc gcc aaa gaa cct att gtt tcc gct tat tat cac gct tcg att gtt   486
Ile Ala Lys Glu Pro Ile Val Ser Ala Tyr Tyr His Ala Ser Ile Val
                 140                 145                 150

tct cag cgt tcg ttg gaa gct gcg ttg gcg aat act tta tct gtt aaa   534
Ser Gln Arg Ser Leu Glu Ala Ala Leu Ala Asn Thr Leu Ser Val Lys
             155                 160                 165

ctc agc aat ttg aat ctt cca agc aac acg ctt ttc gat ttg ttc tct   582
Leu Ser Asn Leu Asn Leu Pro Ser Asn Thr Leu Phe Asp Leu Phe Ser
170                 175                 180

ggt gtt ctt caa gga aac cca gat att gtt gaa tct gtc aag cta gat   630
Gly Val Leu Gln Gly Asn Pro Asp Ile Val Glu Ser Val Lys Leu Asp
185                 190                 195                 200

ctt tta gct gtt aag gag aga gat cct gct tgt ata agc tac gtt cat   678
```

12

Leu Leu Ala Val Lys Glu Arg Asp Pro Ala Cys Ile Ser Tyr Val His
             205   210   215

tgt ttc ctt cac ttt aaa ggc ttc ctc gct tgt caa gcg cat cgt att   726
Cys Phe Leu His Phe Lys Gly Phe Leu Ala Cys Gln Ala His Arg Ile
             220   225   230

gct cat gag ctt tgg act cag gac aga aaa atc cta gct ttg ttg atc   774
Ala His Glu Leu Trp Thr Gln Asp Arg Lys Ile Leu Ala Leu Leu Ile
             235   240   245

cag aac aga gtc tct gaa gcc ttc gct gtt gat ttc cac cct gga gct   822
Gln Asn Arg Val Ser Glu Ala Phe Ala Val Asp Phe His Pro Gly Ala
             250   255   260

aaa atc ggt acc ggg att ttg cta gac cat gct acg gct att gtg atc   870
Lys Ile Gly Thr Gly Ile Leu Leu Asp His Ala Thr Ala Ile Val Ile
265   270   275   280

ggt gag acg gcg gtt gtg ggg aac aat gtt tcg att ctc cat aac gtt   918
Gly Glu Thr Ala Val Val Gly Asn Asn Val Ser Ile Leu His Asn Val
             285   290   295

acg ctt gga gga acg ggg aaa cag tgt gga gat agg cac ccg aag att   966
Thr Leu Gly Gly Thr Gly Lys Gln Cys Gly Asp Arg His Pro Lys Ile
             300   305   310

ggc gat ggg gtt ttg att gga gct ggg act tgt att ttg ggg aat atc   1014
Gly Asp Gly Val Leu Ile Gly Ala Gly Thr Cys Ile Leu Gly Asn Ile
             315   320   325

acg att ggt gaa gga gct aag att ggt gcg ggg tcg gtg gtg ttg aaa   1062
Thr Ile Gly Glu Gly Ala Lys Ile Gly Ala Gly Ser Val Val Leu Lys
             330   335   340

gac gtg ccg ccg cgt acg acg gct gtt gga aat ccg gcg agg ttg ctt   1110
Asp Val Pro Pro Arg Thr Thr Ala Val Gly Asn Pro Ala Arg Leu Leu
345   350   355   360

ggt ggt aaa gat aat ccg aaa acg cat gac aag att cct ggt ttg act   1158
Gly Gly Lys Asp Asn Pro Lys Thr His Asp Lys Ile Pro Gly Leu Thr
             365   370   375

atg gac cag acg tcg cat ata tcc gag tgg tcg gat tat gta att   1203
Met Asp Gln Thr Ser His Ile Ser Glu Trp Ser Asp Tyr Val Ile
             380   385   390

tgaaaaagtc   1213

13

<210> 8
<211> 391
<212> PRT
<213> Arabidopsis thaliana

<400> 8

```
Met Leu Pro Val Thr Ser Arg Arg His Phe Thr Met Ser Leu Tyr Met
1               5                   10                  15

Leu Arg Ser Ser Ser Pro His Ile Asn His His Ser Phe Leu Leu Pro
                20                  25                  30

Ser Phe Val Ser Ser Lys Phe Lys His His Thr Leu Ser Pro Pro Pro
            35                  40                  45

Ser Pro Pro Pro Pro Pro Pro Met Ala Ala Cys Ile Asp Thr Cys Arg
        50                  55                  60

Thr Gly Lys Pro Gln Ile Ser Pro Arg Asp Ser Ser Lys His His Asp
65                  70                  75                  80

Asp Glu Ser Gly Phe Arg Tyr Met Asn Tyr Phe Arg Tyr Pro Asp Arg
                85                  90                  95

Ser Ser Phe Asn Gly Thr Gln Thr Lys Thr Leu His Thr Arg Pro Leu
            100                 105                 110

Leu Glu Asp Leu Asp Arg Asp Ala Glu Val Asp Asp Val Trp Ala Lys
        115                 120                 125

Ile Arg Glu Glu Ala Lys Ser Asp Ile Ala Lys Glu Pro Ile Val Ser
    130                 135                 140

Ala Tyr Tyr His Ala Ser Ile Val Ser Gln Arg Ser Leu Glu Ala Ala
145                 150                 155                 160

Leu Ala Asn Thr Leu Ser Val Lys Leu Ser Asn Leu Asn Leu Pro Ser
                165                 170                 175

Asn Thr Leu Phe Asp Leu Phe Ser Gly Val Leu Gln Gly Asn Pro Asp
                180                 185                 190

Ile Val Glu Ser Val Lys Leu Asp Leu Leu Ala Val Lys Glu Arg Asp
            195                 200                 205

Pro Ala Cys Ile Ser Tyr Val His Cys Phe Leu His Phe Lys Gly Phe
```

14

Leu Ala Cys Gln Ala His Arg Ile Ala His Glu Leu Trp Thr Gln Asp
225   230   235   240

Arg Lys Ile Leu Ala Leu Leu Ile Gln Asn Arg Val Ser Glu Ala Phe
                    245   250   255

Ala Val Asp Phe His Pro Gly Ala Lys Ile Gly Thr Gly Ile Leu Leu
                    260   265   270

Asp His Ala Thr Ala Ile Val Ile Gly Glu Thr Ala Val Val Gly Asn
                    275   280   285

Asn Val Ser Ile Leu His Asn Val Thr Leu Gly Gly Thr Gly Lys Gln
          290   295   300

Cys Gly Asp Arg His Pro Lys Ile Gly Asp Gly Val Leu Ile Gly Ala
305   310   315   320

Gly Thr Cys Ile Leu Gly Asn Ile Thr Ile Gly Glu Gly Ala Lys Ile
                    325   330   335

Gly Ala Gly Ser Val Val Leu Lys Asp Val Pro Pro Arg Thr Thr Ala
               340   345   350

Val Gly Asn Pro Ala Arg Leu Leu Gly Gly Lys Asp Asn Pro Lys Thr
          355   360   365

His Asp Lys Ile Pro Gly Leu Thr Met Asp Gln Thr Ser His Ile Ser
     370   375   380

Glu Trp Ser Asp Tyr Val Ile
385   390

<210> 9
<211> 1080
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (1)..(1080)

<220>
<221> transit_peptide
<222> (1)..(96)

<400> 9

```
atg gtg gat cta tct tcc ttt agc ctc ctt ttt gct ttc tcc gtc tct    48
Met Val Asp Leu Ser Ser Phe Ser Leu Leu Phe Ala Phe Ser Val Ser
 1               5                  10                  15

ctc tct ttt gtc caa tca aaa aga gtt tgt gat tct tct tta tcg tct    96
Leu Ser Phe Val Gln Ser Lys Arg Val Cys Asp Ser Ser Leu Ser Ser
                20                  25                  30

cct tgg aga gat atg aat ggc gat gag ctt cct ttc gag agt ggt ttc   144
Pro Trp Arg Asp Met Asn Gly Asp Glu Leu Pro Phe Glu Ser Gly Phe
            35                  40                  45

gag gtt tac gct aag gga act cat aag tca gag ttt gac tcg aat ttg   192
Glu Val Tyr Ala Lys Gly Thr His Lys Ser Glu Phe Asp Ser Asn Leu
        50                  55                  60

ctt gat cct cgt tct gat cct att tgg gat gct ata aga gaa gaa gct   240
Leu Asp Pro Arg Ser Asp Pro Ile Trp Asp Ala Ile Arg Glu Glu Ala
65                  70                  75                  80

aaa ctt gag gca gag aaa gag cct att ttg agt agc ttc ttg tat gct   288
Lys Leu Glu Ala Glu Lys Glu Pro Ile Leu Ser Ser Phe Leu Tyr Ala
                85                  90                  95

ggt atc tta gca cat gat tgt tta gag caa gct tta ggg ttt gtt cta   336
Gly Ile Leu Ala His Asp Cys Leu Glu Gln Ala Leu Gly Phe Val Leu
            100                 105                 110

gcc aac cgt ctc caa aac cca acc ttg ttg gca aca caa ctc ttg gat   384
Ala Asn Arg Leu Gln Asn Pro Thr Leu Leu Ala Thr Gln Leu Leu Asp
        115                 120                 125

ata ttt tat ggt gtt atg atg cat gac aaa ggt att cag agt tcg att   432
Ile Phe Tyr Gly Val Met Met His Asp Lys Gly Ile Gln Ser Ser Ile
        130                 135                 140

cgc cat gat ctc cag gca ttt aaa gat cgt gat cct gct tgt ctg tcg   480
Arg His Asp Leu Gln Ala Phe Lys Asp Arg Asp Pro Ala Cys Leu Ser
145                 150                 155                 160

tat agt tct gct att tta cat ctg aag ggt tat cat gcg tta caa gca   528
Tyr Ser Ser Ala Ile Leu His Leu Lys Gly Tyr His Ala Leu Gln Ala
                165                 170                 175

tat agg gtt gcg cat aaa ctg tgg aat gaa ggg agg aaa cta tta gct   576
Tyr Arg Val Ala His Lys Leu Trp Asn Glu Gly Arg Lys Leu Leu Ala
```

```
ctt gca ttg caa agc cga ata agc gag gtt ttt ggc att gac ata cat    624
Leu Ala Leu Gln Ser Arg Ile Ser Glu Val Phe Gly Ile Asp Ile His
        195                 200                 205

cca gcg gca aga att ggg gag gga ata ttg ttg gat cat gga act gga    672
Pro Ala Ala Arg Ile Gly Glu Gly Ile Leu Leu Asp His Gly Thr Gly
    210                 215                 220

gtg gtc att ggt gag acc gct gtg ata ggc aac ggt gtc tcg atc tta    720
Val Val Ile Gly Glu Thr Ala Val Ile Gly Asn Gly Val Ser Ile Leu
225                 230                 235                 240

cat ggt gtg act tta gga gga acc gga aag gaa act ggc gat cgc cac    768
His Gly Val Thr Leu Gly Gly Thr Gly Lys Glu Thr Gly Asp Arg His
                245                 250                 255

cca aag ata ggt gaa ggt gca ttg ctt gga gct tgt gtg act ata ctt    816
Pro Lys Ile Gly Glu Gly Ala Leu Leu Gly Ala Cys Val Thr Ile Leu
        260                 265                 270

ggt aac ata agc ata ggt gct gga gca atg gta gct gca ggt tca ctt    864
Gly Asn Ile Ser Ile Gly Ala Gly Ala Met Val Ala Ala Gly Ser Leu
        275                 280                 285

gtg tta aaa gac gtt cct tcg cat agt gtg gtg gct gga aat cct gca    912
Val Leu Lys Asp Val Pro Ser His Ser Val Val Ala Gly Asn Pro Ala
    290                 295                 300

aaa ctg atc agg gtc atg gaa gag caa gac ccg tct cta gca atg aaa    960
Lys Leu Ile Arg Val Met Glu Glu Gln Asp Pro Ser Leu Ala Met Lys
305                 310                 315                 320

cac gat gct act aaa gag ttc ttt cga cat gta gct gat ggt tac aaa    1008
His Asp Ala Thr Lys Glu Phe Phe Arg His Val Ala Asp Gly Tyr Lys
                325                 330                 335

ggg gca caa tct aac gga cca tca ctt tca gca gga gat aca gag aaa    1056
Gly Ala Gln Ser Asn Gly Pro Ser Leu Ser Ala Gly Asp Thr Glu Lys
                340                 345                 350

gga cac act aac agc aca tca tga                                    1080
Gly His Thr Asn Ser Thr Ser
        355                 360
```

<210> 10

<211> 359
<212> PRT
<213> Arabidopsis thaliana

<400> 10
Met Val Asp Leu Ser Ser Phe Ser Leu Leu Phe Ala Phe Ser Val Ser
1   5   10   15

Leu Ser Phe Val Gln Ser Lys Arg Val Cys Asp Ser Ser Leu Ser Ser
            20   25   30

Pro Trp Arg Asp Met Asn Gly Asp Glu Leu Pro Phe Glu Ser Gly Phe
            35   40   45

Glu Val Tyr Ala Lys Gly Thr His Lys Ser Glu Phe Asp Ser Asn Leu
        50   55   60

Leu Asp Pro Arg Ser Asp Pro Ile Trp Asp Ala Ile Arg Glu Glu Ala
65   70   75   80

Lys Leu Glu Ala Glu Lys Glu Pro Ile Leu Ser Ser Phe Leu Tyr Ala
                85   90   95

Gly Ile Leu Ala His Asp Cys Leu Glu Gln Ala Leu Gly Phe Val Leu
                100   105   110

Ala Asn Arg Leu Gln Asn Pro Thr Leu Leu Ala Thr Gln Leu Leu Asp
        115   120   125

Ile Phe Tyr Gly Val Met Met His Asp Lys Gly Ile Gln Ser Ser Ile
        130   135   140

Arg His Asp Leu Gln Ala Phe Lys Asp Arg Asp Pro Ala Cys Leu Ser
145   150   155   160

Tyr Ser Ser Ala Ile Leu His Leu Lys Gly Tyr His Ala Leu Gln Ala
                165   170   175

Tyr Arg Val Ala His Lys Leu Trp Asn Glu Gly Arg Lys Leu Leu Ala
            180   185   190

Leu Ala Leu Gln Ser Arg Ile Ser Glu Val Phe Gly Ile Asp Ile His
        195   200   205

Pro Ala Ala Arg Ile Gly Glu Gly Ile Leu Leu Asp His Gly Thr Gly
        210   215   220

Val Val Ile Gly Glu Thr Ala Val Ile Gly Asn Gly Val Ser Ile Leu

18

His Gly Val Thr Leu Gly Gly Thr Gly Lys Glu Thr Gly Asp Arg His
       245   250   255

Pro Lys Ile Gly Glu Gly Ala Leu Leu Gly Ala Cys Val Thr Ile Leu
       260   265   270

Gly Asn Ile Ser Ile Gly Ala Gly Ala Met Val Ala Ala Gly Ser Leu
     275   280   285

Val Leu Lys Asp Val Pro Ser His Ser Val Val Ala Gly Asn Pro Ala
   290   295   300

Lys Leu Ile Arg Val Met Glu Glu Gln Asp Pro Ser Leu Ala Met Lys
305   310   315   320

His Asp Ala Thr Lys Glu Phe Phe Arg His Val Ala Asp Gly Tyr Lys
       325   330   335

Gly Ala Gln Ser Asn Gly Pro Ser Leu Ser Ala Gly Asp Thr Glu Lys
     340   345   350

Gly His Thr Asn Ser Thr Ser
     355

<210> 11
<211> 900
<212> DNA
<213> Arabidopsis thaliana

<220>
<221> CDS
<222> (1)..(900)

<220>
<221> transit_peptide
<222> (1)..(90)

<400> 11
atg gct tgt ata aac ggc gag aat cgt gat ttt tct tcc tcg tca tct 48
Met Ala Cys Ile Asn Gly Glu Asn Arg Asp Phe Ser Ser Ser Ser Ser
 1   5   10   15

ttg tct tct ctt cca atg att gtc tcc cgg aac ttt tct gcc aga gac 96
Leu Ser Ser Leu Pro Met Ile Val Ser Arg Asn Phe Ser Ala Arg Asp
     20   25   30

```
gat gga gag acc ggt gac gag ttt cct ttc gag agg att ttc ccg gtt    144
Asp Gly Glu Thr Gly Asp Glu Phe Pro Phe Glu Arg Ile Phe Pro Val
         35                  40                  45

tac gct aga gga acc ctt aat ccc gtg gcc gac ccg gtt ttg ctg gat    192
Tyr Ala Arg Gly Thr Leu Asn Pro Val Ala Asp Pro Val Leu Leu Asp
         50                  55                  60

ttt acc aat tct agt tat gac cca att tgg gat tct ata aga gaa gaa    240
Phe Thr Asn Ser Ser Tyr Asp Pro Ile Trp Asp Ser Ile Arg Glu Glu
 65                  70                  75                  80

gct aag ctt gag gca gaa gag gag ccg gtt ttg agt agc ttc ttg tat    288
Ala Lys Leu Glu Ala Glu Glu Glu Pro Val Leu Ser Ser Phe Leu Tyr
                 85                  90                  95

gct agt atc ttg tcg cat gac tgt tta gag caa gca ttg agt ttt gtt    336
Ala Ser Ile Leu Ser His Asp Cys Leu Glu Gln Ala Leu Ser Phe Val
                100                 105                 110

cta gct aac cgt ctc caa aac cct acc ttg ttg gca act cag ctt atg    384
Leu Ala Asn Arg Leu Gln Asn Pro Thr Leu Leu Ala Thr Gln Leu Met
            115                 120                 125

gat ata ttt tgc aac gtt atg gta cat gac aga ggt att caa agc tcg    432
Asp Ile Phe Cys Asn Val Met Val His Asp Arg Gly Ile Gln Ser Ser
        130                 135                 140

att cgt ctt gat gtt cag gca ttc aaa gac aga gat cct gct tgt cta    480
Ile Arg Leu Asp Val Gln Ala Phe Lys Asp Arg Asp Pro Ala Cys Leu
145                 150                 155                 160

tcg tat agt tcg gct att tta cat ctg aag ggc tat ctt gca ctg cag    528
Ser Tyr Ser Ser Ala Ile Leu His Leu Lys Gly Tyr Leu Ala Leu Gln
            165                 170                 175

gcg tat aga gta gca cat aag ttg tgg aag caa gga aga aaa cta tta    576
Ala Tyr Arg Val Ala His Lys Leu Trp Lys Gln Gly Arg Lys Leu Leu
            180                 185                 190

gca ttg gca ctg caa agc cga gta agc gag gta aga act gct gtg ata    624
Ala Leu Ala Leu Gln Ser Arg Val Ser Glu Val Arg Thr Ala Val Ile
            195                 200                 205

ggc gac cgt gtc tca att ttg cat ggt gtg aca tta gga gga act ggg    672
Gly Asp Arg Val Ser Ile Leu His Gly Val Thr Leu Gly Gly Thr Gly
    210                 215                 220
```

```
aaa gaa acc ggt gac cgc cat cca aat ata ggc gac ggt gct ctt ctt      720
Lys Glu Thr Gly Asp Arg His Pro Asn Ile Gly Asp Gly Ala Leu Leu
225                 230                 235                 240

gga gca tgt gtg act ata ctt ggt aac att aag ata ggc gct gga gca      768
Gly Ala Cys Val Thr Ile Leu Gly Asn Ile Lys Ile Gly Ala Gly Ala
            245                 250                 255

atg gta gct gct ggt tcg ctt gtg tta aag gat gtt cct tcg cat agc      816
Met Val Ala Ala Gly Ser Leu Val Leu Lys Asp Val Pro Ser His Ser
        260                 265                 270

atg gtg gct gga aat cca gca aaa ctc atc ggg ttt gtt gat gag caa      864
Met Val Ala Gly Asn Pro Ala Lys Leu Ile Gly Phe Val Asp Glu Gln
        275                 280                 285

gat cca tct atg aca atg gag cat ggt gag tct tga                      900
Asp Pro Ser Met Thr Met Glu His Gly Glu Ser
290                 295                 300


<210> 12
<211> 299
<212> PRT
<213> Arabidopsis thaliana

<400> 12
Met Ala Cys Ile Asn Gly Glu Asn Arg Asp Phe Ser Ser Ser Ser Ser
1               5                   10                  15

Leu Ser Ser Leu Pro Met Ile Val Ser Arg Asn Phe Ser Ala Arg Asp
            20                  25                  30

Asp Gly Glu Thr Gly Asp Glu Phe Pro Phe Glu Arg Ile Phe Pro Val
        35                  40                  45

Tyr Ala Arg Gly Thr Leu Asn Pro Val Ala Asp Pro Val Leu Leu Asp
    50                  55                  60

Phe Thr Asn Ser Ser Tyr Asp Pro Ile Trp Asp Ser Ile Arg Glu Glu
65                  70                  75                  80

Ala Lys Leu Glu Ala Glu Glu Glu Pro Val Leu Ser Ser Phe Leu Tyr
                85                  90                  95

Ala Ser Ile Leu Ser His Asp Cys Leu Glu Gln Ala Leu Ser Phe Val
        100                 105                 110
```

21

```
Leu Ala Asn Arg Leu Gln Asn Pro Thr Leu Leu Ala Thr Gln Leu Met
        115                 120                 125

Asp Ile Phe Cys Asn Val Met Val His Asp Arg Gly Ile Gln Ser Ser
        130                 135                 140

Ile Arg Leu Asp Val Gln Ala Phe Lys Asp Arg Asp Pro Ala Cys Leu
145                 150                 155                 160

Ser Tyr Ser Ser Ala Ile Leu His Leu Lys Gly Tyr Leu Ala Leu Gln
                165                 170                 175

Ala Tyr Arg Val Ala His Lys Leu Trp Lys Gln Gly Arg Lys Leu Leu
                180                 185                 190

Ala Leu Ala Leu Gln Ser Arg Val Ser Glu Val Arg Thr Ala Val Ile
        195                 200                 205

Gly Asp Arg Val Ser Ile Leu His Gly Val Thr Leu Gly Gly Thr Gly
        210                 215                 220

Lys Glu Thr Gly Asp Arg His Pro Asn Ile Gly Asp Gly Ala Leu Leu
225                 230                 235                 240

Gly Ala Cys Val Thr Ile Leu Gly Asn Ile Lys Ile Gly Ala Gly Ala
                245                 250                 255

Met Val Ala Ala Gly Ser Leu Val Leu Lys Asp Val Pro Ser His Ser
        260                 265                 270

Met Val Ala Gly Asn Pro Ala Lys Leu Ile Gly Phe Val Asp Glu Gln
        275                 280                 285

Asp Pro Ser Met Thr Met Glu His Gly Glu Ser
    290                 295


<210> 13
<211> 54
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
      Oligonucleotide

<400> 13
```

gagagaggat cctctttcca atcataaacc atggcaacat gcatagacac atgc   54

<210> 14
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
      Oligonucleotide

<400> 14
ggctcaccag actaatacac taaattgtgt ttacctcgag agagag   46

<210> 15
<211> 52
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Synthetic
      Oligonucleotide

<400> 15
gagagaggat cctcttatcg ccgcgttaat atgccaccgg ccggagaact cc   52

<210> 16
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence

<400> 16
gagccttacc agtctaatgt agtatatttc aacctcgaga gagag   45

<210> 17
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence

23

<400> 17

gagagaggat cccctcctcc tcctcctcct atggctgcgt gcatcgacac ctg   53

<210> 18
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence

<400> 18

gctcaccagc ctaatacatt aaactttttc agctcgagag agag   44

<210> 19
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence

<220>
<223> Description of Artificial Sequence

<400> 19

gagagaggat ccggccgaga aaaaaaaaaa atgttgccgg tcacaagtcg ccg   53

<210> 20
<211> 49
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence

<400> 20

gagagaggat ccgacaagtt ggcataattt atggtggatc tatcttcct   49

<210> 21
<211> 43
<212> DNA
<213> Artificial Sequence

24

<220>
<223> Description of Artificial Sequence

<220>
<223> Description of Artificial Sequence

<400> 21
cctgtgtgat tgtcgtgtag tactctagaa actcgagaga gag   43

<210> 22
<211> 67
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence

<400> 22
gagagaggat ccgacaagtt ggcataattt atggcttgta taaacggcga gaatcgtgat 60

ttttctt   67

<210> 23
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence

<400> 23
tacctcgtac cactcagaac tctagaaact cgagagagag   40